SEQUENCE LISTING

<110> Grainger, David J.
      Tatalick, Lauren Marie

<120> Compounds and methods to inhibit or
  augment an inflammatory response.

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<140> US 08/927939
<141> 1997-09-11

<160> 85

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                20                  25                  30
Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
            35                  40                  45
Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
        50                  55                  60
Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
65                  70                  75                  80
Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
                85                  90                  95
Pro Lys Thr


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<212> PRT
<213> Homo sapiens

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Thr Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg
            35                  40                  45
Gly Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser
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<212> PRT
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Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu
         35   40   45
Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val
         50   55   60
Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
65   70   75   80
Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr
             85   90   95
Pro Lys Leu

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Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
         35   40   45
Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
         50   55   60
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65   70   75   80
Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
             85   90

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             20   25   30
Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val
         35   40   45
Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val
         50   55   60
Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser
65   70   75   80
Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
             85   90

4

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<213> Homo sapiens

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Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
            20                  25                  30
Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
        35                  40                  45
Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe
    50                  55                  60
Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp
65                  70                  75                  80
Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser
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<213> Homo sapiens

<400> 22
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            20                  25                  30
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
        35                  40                  45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
    50                  55                  60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65                  70                  75                  80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys
                85
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<213> Homo sapiens

<400> 23
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Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
            20                  25                  30
Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
        35                  40                  45
Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
    50                  55                  60
Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
65                  70                  75                  80
Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala
                85                  90                  95
Glu Asn Ser
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<213> Homo sapiens

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        20   25   30
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
        35   40   45
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
        50   55   60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65   70   75   80
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
                85   90   95
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
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<210> 25
<211> 97
<212> PRT
<213> Homo sapiens

<400> 25
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Phe Ser Pro Gln Gly Leu Ala Gly Pro Ala Ser Val Pro Thr Thr Cys
        20   25   30
Cys Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser
        35   40   45
Tyr Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe
        50   55   60
Lys Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp
65   70   75   80
Val Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys
                85   90   95
Pro

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<400> 26
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            20   25   30
Thr Cys Cys Tyr Ser Phe Thr Ser Lys Met Ile Pro Met Ser Arg Leu
            35   40   45
Glu Ser Tyr Lys Arg Ile Thr Ser Ser Arg Cys Pro Lys Glu Ala Val
        50   55   60
Val Phe Val Thr Lys Leu Lys Arg Glu Val Cys Ala Asp Pro Lys Lys
65   70   75   80
Glu Trp Val Gln Thr Tyr Ile Lys Asn Leu Asp Arg Asn Gln Met Arg
                85   90   95
Ser Glu Pro Thr Thr Leu Phe Lys Thr Ala Ser Ala Leu Arg Ser Ser
            100   105   110
Ala Pro Leu Asn Val Lys Leu Thr Arg Lys Ser Glu Ala Asn Ala Ser
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6

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Val Thr Val Asn
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<210> 28
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Leu Cys Leu Leu Leu Met Thr Ala Ala Phe Asn Pro Gln Gly Leu Ala
        10              15              20


cag cca gat gca ctc aac gtc cca tct act tgc tgc ttc aca ttt agc        150
Gln Pro Asp Ala Leu Asn Val Pro Ser Thr Cys Cys Phe Thr Phe Ser
    25              30              35


agt aag aag atc tcc ttg cag agg ctg aag agc tat gtg atc acc acc        198
Ser Lys Lys Ile Ser Leu Gln Arg Leu Lys Ser Tyr Val Ile Thr Thr
    40              45              50                  55


agc agg tgt ccc cag aag gct gtc atc ttc aga acc aaa ctg ggc aag        246
Ser Arg Cys Pro Gln Lys Ala Val Ile Phe Arg Thr Lys Leu Gly Lys
                60              65                  70


gag atc tgt gct gac cca aag gag aag tgg gtc cag aat tat atg aaa        294
Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln Asn Tyr Met Lys
                75              80                  85


cac ctg ggc cgg aaa gct cac acc ctg aag act tgaactctgc tacccctact     347
His Leu Gly Arg Lys Ala His Thr Leu Lys Thr
                90              95


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                     Met Asn Ala Lys Val Val Val Val Leu Val Leu
                      1               5                  10

gtg ctg acc gcg ctc tgc ctc agc gac ggg aag ccc gtc agc ctg agc      160
Val Leu Thr Ala Leu Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser
            15                  20                  25

tac aga tgc cca tgc cga ttc ttc gaa agc cat gtt gcc aga gcc aac      208
Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn
        30                  35                  40

gtc aag cat ctc aaa att ctc aac act cca aac tgt gcc ctt cag att      256
Val Lys His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile
    45                  50                  55

gta gcc cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aag      304
Val Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
60                  65                  70                  75

cta aag tgg att cag gag tac ctg gag aaa gct tta aac aag agg ttc      352
Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe
                80                  85                  90

aag atg tgagagggtc agacgcctga ggaaccctta cagtaggagc ccagctctga      408
Lys Met


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8

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9

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                                  Met Asn Pro Ser Ala Ala Val Ile
                                   1               5

ttc tgc ctc atc ctg ctg ggt ctg agt ggg act caa g gtaagggaca   2140
Phe Cys Leu Ile Leu Leu Gly Leu Ser Gly Thr Gln
 10              15              20

ccaaggccat ttaattaacg aagtcagaag tcagacgatt aagctcagtt ctaaacacag   2200
catgtattta agctttaatg tgtgtaccta taagaagag ggaagcagga agaaatccct   2260
tcagcttgca gagtttatca taggctggtt gaagtcagag aaaaatagaa taaaagaaaa   2320
ggaacgaaga agggaagaaa gggagaaaag gaggagggag gaggaagaag agggaagag   2380
agagtcagga gaaagggcga aagagtggga tggggtaagg catggatgcc tccttgcctg   2440
agcctaacca atactgtgag cagtgcataa atgcaggatt tcgtaactga caagttgcag   2500
atctctcttt accatgacca agatattcaa acactcagcc ctatgatacg atgggatgcg   2560
tctctccaca gatcagacag ggtctgctaa acactacctc atccatttta agtgcctaaa   2620
atgaaaccgt gtgctgacct tcctggctct cccctctct tcctgcag gg atc cct   2676
                                                  Gly Ile Pro


ctc gca agg acg gtc cgc tgc aac tgc atc cat atc gat gac ggg cca   2724
Leu Ala Arg Thr Val Arg Cys Asn Cys Ile His Ile Asp Asp Gly Pro
 25              30              35

gtg aga atg agg gcc ata ggg aag ctt gaa atc atc cct gcg agc cta   2772
Val Arg Met Arg Ala Ile Gly Lys Leu Glu Ile Ile Pro Ala Ser Leu
 40              45              50              55

tcc tgc cca cgt gtt gag atc at gtgagtacaa gcccacctgc cgataaacgt   2825
Ser Cys Pro Arg Val Glu Ile Ile
                60

ccctcccgta accacacagt aaataagtga gggaaaccag gaaagatggg gacgggtctg   2885
tgactctaac taaggcacag tgcctgaact ctgacatgga cctgcagggc catcagctct   2945
gttggcctga cgttaatctg agtatctcac tcttatttct atag t gcc acg atg   2999
                                               Ala Thr Met
                                                    65


aaa aag aat gat gag cag aga tgt ctg aat ccg gaa tct aag acc atc   3047
Lys Lys Asn Asp Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys Thr Ile
 70              75              80
```

10

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aag aat tta atg aaa gcg ttt agc caa aaa ag gtaggtttga tgttgctttt      3099
Lys Asn Leu Met Lys Ala Phe Ser Gln Lys Arg
          85                  90


tcaggaaatg gtggtctggg gagcagcgcc tgccctgggc tttgctgtgg gcatctgccc      3159
taaactcatg gcaccggcat gtgcctttgt ctctccattt acacagacac tgaggtgcct      3219
tcttaggtca tacattccta gtgtctagaa gtggagcagt tattatacct gtcacgggta      3279
aagctgccaa atgcccaccc ccccacttcc tcacttaaaa aaaaaaaacc aaaaacaaac      3339
aaacccattc tgtcccctca acccccaccc accgtgacc catggagatt gtgtagcaga      3399
ggaaaatgca ccaggccttt tgccccaggg tctttgggtt ccaaagtgaa agcagagtct      3459
atccgctcaa tacagtttcc tcttcctaca g g tct aaa agg gct cct            3506
                                    Ser Lys Arg Ala Pro
                                             95


taactggaga gaagccacgc acacaccccg gtgctgtgat ggacagcaga gagcctgtct      3566
ctccatcact ccccctttacc cagtggatgg ctagtcctaa ttgcccttgg tcttctgaaa      3626
ggtgaccagc cgtggtcaca tcagctgcta ctcctcctgc aggatgatgg ttaagccatg      3686
gtcctgagac aaaagtaact gccgaagcaa gaattcttta agggctggtc tgagtcctca      3746
ctcaagtggc tgggatggct gtcctagctc tgtactgtaa gctatgtgga ggtgcgacgc      3806
ccttcaccat gtgccacgcc ccaggctgct ccccacaccc tccttgtcct ccctagctca      3866
ggctcgtcag ttctgagttt acctgagctc ttttatttca gatgtaagac tacaaattta      3926
agtttgtaag acaaacttaa ccaccatct tcccaagggg ttatcaagat actcagagga      3986
acctggaaat gtatgtgtaa atactattta atgaacgact gtacaaagta gaattcctag      4046
atgtatttt tgtatgcttt gcattgtata tggaagaact tgtgtcatca agtatgtatc      4106
aatgggtagt taaagtttat ttttaaaacc gtccaatacc ttttgtatta tgtaacattc      4166
aaaagacaat gtactgtatt gaaagtagta agagacccaa aatgtaataa agtaataata      4226
actgacatga aatggtcatg tgactgagaa ttc                                4259


<210> 31
<211> 1081
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (43)...(363)

<400> 31
ctctcctcct cgcacagccg ctcgaaccgc ctgctgagcc cc atg gcc cgc gcc        54
                                              Met Ala Arg Ala
                                               1


acg ctc tcc gcc gcc ccc agc aat ccc cgg ctc ctg cgg gtg gcg ctg      102
Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu Arg Val Ala Leu
 5              10              15                      20


ctg ctc ctg ctc ctg gtg gcc gcc agc cgg cgc gca gca gga gcg ccc      150
Leu Leu Leu Leu Leu Val Ala Ala Ser Arg Arg Ala Ala Gly Ala Pro
               25              30                      35


ctg gcc act gaa ctg cgc tgc cag tgc ttg cag acc ctg cag gga att      198
Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln Gly Ile
             40              45              50


cac ctc aag aac atc caa agt gtg aag gtg aag tcc ccc gga ccc cac      246
His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser Pro Gly Pro His
          55              60              65


tgc gcc caa acc gaa gtc ata gcc aca ctc aag aat ggg cag aaa gct      294
Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Gln Lys Ala
       70              75              80
```

11

```
tgt ctc aac ccc gca tcg ccc atg gtt aag aaa atc atc gaa aag atg          342
Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile Ile Glu Lys Met
 85                  90                  95                 100

ctg aaa aat ggc aaa tcc aac tgaccagaag gaaggaggaa gcttattggt            393
Leu Lys Asn Gly Lys Ser Asn
                105

ggctgttcct gaaggaggcc ctgcccttac aggaacagaa gaggaaagag agacacagct       453
gcagaggcca cctggattgc gcctaatgtg tttgagcatc acttaggaga agtcttctat       513
ttatttattt atttatttat ttgtttgttt tagaagattc tatgttaata ttttatgtgt       573
aaaataaggt tatgattgaa tctacttgca cactctccca ttatatttat tgtttatttt       633
aggtcaaacc caagttagtt caatcctgat tcatatttaa tttgaagata gaaggtttgc       693
agatattctc tagtcatttg ttaatatttc ttcgtgatga catatcacat gtcagccact       753
gtgatagagg ctgaggaatc caagaaaatg gccagtgaga tcaatgtgac ggcagggaaa       813
tgtatgtgtg tctattttgt aactgtaaag atgaatgtca gttgttattt attgaaatga       873
tttcacagtg tgtggtcaac atttctcatg ttgaagcttt aagaactaaa atgttctaaa       933
tatcccttgg acattttatg tctttcttgt aaggcatact gccttgttta atgttaatta       993
tgcagtgttt ccctctgtgt tagagcagag aggtttcgat atttattgat gttttcacaa      1053
agaacaggaa aataaatat ttaaaaat                                          1081
```

<210> 32
<211> 1173
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (107)...(448)

<400> 32

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cggcacgagc acagtgctcc ggatcctcca atcttcgctc ctccaatctc cgctcctcca           60
cccagttcag gaacccgcga ccgctcgcag cgctctcttg accact atg agc ctc              115
                                                      Met Ser Leu
                                                       1

ctg tcc agc cgc gcg gcc cgt gtc ccc ggt cct tcg agc tcc ttg tgc         163
Leu Ser Ser Arg Ala Ala Arg Val Pro Gly Pro Ser Ser Ser Leu Cys
 5                  10                  15

gcg ctg ttg gtg ctg ctg ctg ctg ctg acg cag cca ggg ccc atc gcc         211
Ala Leu Leu Val Leu Leu Leu Leu Leu Thr Gln Pro Gly Pro Ile Ala
 20                  25                  30                  35

agc gct ggt cct gcc gct gct gtg ttg aga gag ctg cgt tgc gtt tgt         259
Ser Ala Gly Pro Ala Ala Ala Val Leu Arg Glu Leu Arg Cys Val Cys
                40                  45                  50

tta cag acc acg cag gga gtt cat ccc aaa atg atc agt aat ctg caa         307
Leu Gln Thr Thr Gln Gly Val His Pro Lys Met Ile Ser Asn Leu Gln
                55                  60                  65

gtg ttc gcc ata ggc cca cag tgc tcc aag gtg gaa gtg gta gcc tcc         355
Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser
                70                  75                  80

ctg aag aac ggg aag gaa att tgt ctt gat cca gaa gcc cct ttt cta         403
Leu Lys Asn Gly Lys Glu Ile Cys Leu Asp Pro Glu Ala Pro Phe Leu
 85                  90                  95
```

12

```
aag aaa gtc atc cag aaa att ttg gac ggt gga aac aag gaa aac       448
Lys Lys Val Ile Gln Lys Ile Leu Asp Gly Gly Asn Lys Glu Asn
100             105             110

tgattaagag aaatgagcac gcatggaaaa gtttcccagt ctacagcaga gaagttttct    508
ggaggtctct gaacccaggg aagacaagaa ggaaagattt tgttgttgtt tgtttatttg    568
gtttccccag tagttagctt tcttccctgg attcctcact tttgaagagt gtgaggaaaa    628
cctatgtttg gcgcttaagc tttcagctca gcttaatgaa gtgtttagca tagtacctct    688
gctatttgct gttattttat ctgctatgct attgaagttt tggcaattga ctatagtgtg    748
agccaggaat cactggctgt taatcttaca aagtgtcttg gaattgtagg tgactattat    808
ttttccaaga aatatccctt aagatattaa ctgagaaggc tgggggttta atgtggaaat    868
gatgtttcaa aaggaatcct gtgatggaaa tacaactggt atcttcactt ttttaggaat    928
tgggaaatat tttaatgttt cttggggaat atgttagaga attcccttac tcttgattgt    988
gggatactat ttaattattt cactttagaa agctgagtgt ttcacacctt atctatgtag   1048
aatatatttc cttattcaga atttctaaaa gtttaagttc tatgagggct aatatcttat   1108
cttcctataa ttttagacat tgctttaact ttttagtaaa aaaaaaaaaa aaaaaaaaaa   1168
aaaaa                                                              1173


<210> 33
<211> 825
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (34)...(327)

<400> 33
acattgtgaa atctccaact cttaaccttc aac atg aaa gtc tct gca gtg ctt     54
                                     Met Lys Val Ser Ala Val Leu
                                     1               5

ctg tgc ctg ctg ctc atg aca gca gct ttc aac ccc cag gga ctt gct    102
Leu Cys Leu Leu Leu Met Thr Ala Ala Phe Asn Pro Gln Gly Leu Ala
        10              15                  20

cag cca gat gca ctc aac gtc cca tct act tgc tgc ttc aca ttt agc    150
Gln Pro Asp Ala Leu Asn Val Pro Ser Thr Cys Cys Phe Thr Phe Ser
    25                  30                  35

agt aag aag atc tcc ttg cag agg ctg aag agc tat gtg atc acc acc    198
Ser Lys Lys Ile Ser Leu Gln Arg Leu Lys Ser Tyr Val Ile Thr Thr
40              45                  50                      55

agc agg tgt ccc cag aag gct gtc atc ttc aga acc aaa ctg ggc aag    246
Ser Arg Cys Pro Gln Lys Ala Val Ile Phe Arg Thr Lys Leu Gly Lys
                60                  65                  70

gag atc tgt gct gac cca aag gag aag tgg gtc cag aat tat atg aaa    294
Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln Asn Tyr Met Lys
            75                  80                  85

cac ctg ggc cgg aaa gct cac acc ctg aag act tgaactctgc tacccctact    347
His Leu Gly Arg Lys Ala His Thr Leu Lys Thr
        90                  95

gaaatcaagc tggagtacgt gaaatgactt ttccattctc ctctggcctc ctcttctatg    407
ctttggaata cttctaccat aattttcaaa taggatgcat tcggttttgt gattcaaaat    467
gtactatgtg ttaagtaata ttggctatta tttgacttgt tgctggtttg gagtttattt    527
gagtattgct gatcttttct aaagcaaggc cttgagcaag taggttgctg tctctaagcc    587
cccttccctt ccactatgag ctgctggcag tgggttgtat tcggttccca ggggttgaga    647
gcatgcctgt gggagtcatg gacatgaagg gatgctgcaa tgtaggaagg agagctcttt    707
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13

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gtgaatgtga ggttgttgct aaattattgt ttattgtgga aagatgaatg caatagtagg     767
actgctgaca ttttgcagaa aatacatttt atttaaaatc tcctaaaaaa aaaaaaaa      825


<210> 34
<211> 3112
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1192)...(1267)

<221> CDS
<222> (1953)...(2067)

<221> CDS
<222> (2488)...(2575)


<400> 34
ttagagactt aataataaag gatcttgtgg ataatttatc attccctgat agagaaaaat      60
ttagctttgc ttattttaga gttataaatg atgctgggtc aggtatcttt atgtttgaag     120
atggctccat atttgggttg tttccacaga actctttccc agaaatgctt tttctaggtt     180
aatggctaca catatttcta ggcacctgac atactgacac ccacctctaa agtattttta     240
tgatccacaa ctagcgttta acacagcgcc ccagtcactc cgagactaat aaatagacaa     300
atgactgaaa cgtgacctca tgctttctat tcctccagct ttcattgagt tcctttcctc     360
tgggaggact gggggttgtc tagccctcca cagcatcagc ccattgaccc tatccttgtg     420
gttatagcag ctgaggaagc agaattacag ctctgtggga aggaatgggg ctggagagtt     480
catgcataga ccaattcttt tttttttttt tttttgagat ggagtttcac ttttgttgcc     540
caggctggag tgcaatggca tgatctcagc tcaccacagc ccccacctcc tgggttcaag     600
cgattctcct gccctcagcc tcccgagtag ctgggattac aggcatgtgc caccacgcct     660
gactactttt gtatttttag tagagatgga gtttctcttt cttggtcagg ttggtctcaa     720
actcctgacc tcaggtgatc cgcagcctcg gcctcccaaa gtgttgggat tacaggtgtg     780
agcgaccatg cctggctgca tagaccagtt cttatgagaa gggatcaact aagaatagcc     840
ttgggttgac acacacccct cttcacactc acaggagaaa ccccatgaag ctagaaccag     900
tcatgagttg agagctgaga gttagagagt agctcagaga tgctattctt ggatatcctg     960
agcccctgtg gtcaccaggg accctgagtt gtgcaacact cagcatgaca gcatcactac    1020
acttaaaaat ttccctcctc accccagat tccatttccc catccgccag ggctgcctat    1080
aaagaggaga gatggcttca gacatcagaa ggacgcaggc agcaaagagt agtcagtccc    1140
ttcttggctc tgctgacact cgagcccaca ttccatcacc tgctcccaat c atg cag    1197
                                                          Met Gln
                                                            1


gtc tcc act gct gcc ctt gcc gtc ctc ctc tgc acc atg gct ctc tgc    1245
Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala Leu Cys
         5                   10                  15


aac cag gtc ctc tct gca cca c gtgagtccat gttgttgttg tgggtatcac    1297
Asn Gln Val Leu Ser Ala Pro
         20                  25


cactctctgg ccatggttag accacatcag tcttttttttg cggcctgaga gccccgaaga    1357
gaaaagaagg aagttcttaa agcgctgcca aacaccttgg tcttttttctt cacaactttt    1417
atttttatct ctagaagggg tcttagccct cctagtctcc aggtatgaga atctaggcag    1477
gggcagggga gttacagtcc cttgtacaga tagaaaaaca gggttcaaaa cgaatcagtt    1537
tgcaagaggc agaatccagg gctgcttact tcccagtggg gtctgttgtt cactctccag    1597
ctcaccctag gtctcccagg agccctgtcc cttggatgtc ttatgagaga tgtccagggc    1657
ttctcttggg ctggggtatg acttcttgaa ccgacaaaat tccatgaaga gagctaagag    1717
aacagtccat tcaggtatct ggatcacata gagaaacaga gaacccacta tgaagagtca    1777
agggggaaaga ggaatataga cagaaacaaa gagacatttc tctgcaaaac cccccaaatg    1837
ccttgcagtc acttggtctg agcaagcctg ccctcctcaa ccactcaggg atcagaagct    1897
gcctggcctt ttcttctgag ctgtgactcg ggcttattct ctcctttctc cgcag tt    1954
                                                               Leu
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14

```
gct gct gac acg ccg acc gcc tgc tgc ttc agc tac acc tcc cga cag      2002
Ala Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln
            30                  35                  40

att cca cag aat ttc ata gct gac tac ttt gag acg agc agc cag tgc      2050
Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys
            45                  50                  55

tcc aag ccc agt gtc at gtaagtgcca gtcttcctgc tcacctctag             2097
Ser Lys Pro Ser Val Ile
        60

ggaggtaggg agtgtcaggg tgggggcaga aacaggccag aaggccatcc tggaaaggcc    2157
cagccttcag gagcctatcg gggatacagg acgcagggca ctgaggtgtg acctgacttg    2217
gggctggagt gaggtgggtg ttacagagtc aggaagggct gccccaggcc agaggaaagg    2277
aacaggaaga aggaggcagc aggacactct gagggccccc ttgcctggag tcactgagag    2337
aagctctcta gacggagata ggcagggggc ccctgagaga ggagcaggcc ttgagctgcc    2397
caggacagag agcaggatgt caggccatgg tgggcccagg attccccggc tggattcccc    2457
agtgcttaac tcttcctccc ttctccacag c ttc cta acc aag aga ggc cgg      2509
                                    Phe Leu Thr Lys Arg Gly Arg
                                     65                  70

cag gtc tgt gct gac ccc agt gag gag tgg gtc cag aaa tac gtc agt      2557
Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser
            75                  80                  85

gac ctg gag ctg agt gcc tgaggggtcc agaagcttcg aggcccagcg            2605
Asp Leu Glu Leu Ser Ala
            90

acctcagtgg gcccagtggg gaggagcagg agcctgagcc ttgggaacat gcgtgtgacc    2665
tctacagcta cctcttctat ggactggtta ttgccaaaca gccacactgt gggactcttc    2725
ttaacttaaa ttttaattta tttatactat ttagtttta taatttattt ttgatttcac    2785
agtgtgtttg tgattgtttg ctctgagagt tcccctgtc ccctccacct tccctcacag     2845
tgtgtctggt gacgaccgag tggctgtcat cggcctgtgt aggcagtcat ggcaccaaag    2905
ccaccagact gacaaatgtg tatcagatgc ttttgttcag ggctgtgatc ggcctgggga    2965
aataataaag atgttctttt aaacggtaaa ccagtattga gtttggtttt gtttttctgg    3025
caaatcaaaa tcactagtta agaggaatca taggcaaaga ttaggaagag gtgaaatgga    3085
gggaaactgg gagagatggg gagcgct                                         3112

<210> 35
<211> 481
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (55)...(333)

<400> 35
agcctctgaa gctcccacca ggccagctct cctcccacaa cagcttccca cagc atg      57
                                                              Met
                                                               1

aag atc tcc gtg gct gcc att ccc ttc ttc ctc ctc atc acc atc gcc     105
Lys Ile Ser Val Ala Ala Ile Pro Phe Phe Leu Leu Ile Thr Ile Ala
            5                  10                  15

cta ggg acc aag act gaa tcc tcc tca cgg gga cct tac cac ccc tca     153
Leu Gly Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro Ser
            20                  25                  30
```

6 |

```
gag tgc tgc ttc acc tac act acc tac aag atc ccg cgt cag cgg att        201
Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg Ile
         35              40                  45

atg gat tac tat gag acc aac agc cag tgc tcc aag ccc gga att gtc        249
Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile Val
 50              55                  60                  65

ttc atc acc aaa agg ggc cat tcc gtc tgt acc aac ccc agt gac aag        297
Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp Lys
                 70                  75                  80

tgg gtc cag gac tat atc aag gac atg aag gag aac tgagtgaccc            343
Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn
                 85                  90

agaaggggtg gcgaaggcac agctcagaga cataaagaga agatgccaag gcccctcct      403
ccacccaccc ctaactctca gccccagtca ccctcttgga gcttccctgc tttgaattaa     463
agaccactca tgctcttc                                                    481
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G1

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<400> 36
tctagaaaaa aaaaaacaaa aagggaaaat tcccctggca ggactctcag atgctgctga       60
gtagctctca gtcctctctg taacccaaac ataacacatc tatctccgtg cttacactgg      120
gtggctttca cttgtttatc tgtgaattga agagaagttg cttgaggtca ggcagtgctc      180
ctcattggta actgccttct ctggggctaa ccaaggacct agaacagaat aagctattga      240
aaattgttga ggattgaaaa aaatagaaaa aatagaaatg caaatatct aggccagtca       300
ctggacatag agaatgttat ttaattctta tcgcacgtcc ttgagacatg tattgctatt      360
tgcattttgt gtgaatatgc atttgggtaa gtttatgtaa tccctcctct gcagaactgg      420
gattcaaatg caggtgtatc tctgttcagg tccagactct tctgccctga agcagtagta      480
cttggatgga atgacgtagg gttggacaag ccacacagag gccacttcct ctcacttact      540
tttctttgct tcccactcaa ccaggacagt tcccacgcac tttttcaaga ttcttatctg      600
ctcccacact tggggaagtt cccaatgcaa cctatcaatc catcaccacc acgaatacca      660
gccaggagag gtggggaaag gagtttacca catggtcgct gggtgtgagc aactgttccc      720
tgtccctatg gcttcccact tgtggctccc accatggcct ggagtttgg gtggagtttt       780
tcaaataaaa gccctcagca ttgcaggacg gcacagtggt gagctcttag cttcaccagg      840
ctcatcaaag ctgctccagg aaggcccaag ccagaccaga agac atg cag atc atc      896
                                                     Met Gln Ile Ile
                                                      1

acc aca gcc ctg gtg tgc ttg ctg cta gct ggg atg tgg ccg gaa gat        944
Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met Trp Pro Glu Asp
 5              10                  15                  20

gtg gac agc aag agc a gtgagtgtgg caggcatcat tttgcttctc tctggggagg      1000
Val Asp Ser Lys Ser
                 25
```

16

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gcagaaacgt ggtcagccac tctgggggttg gagcaggctt ctccttgaac tcaccaactc   1060
tatctcccct cttcctacct aaagaggagg aatggtgaac ttggacaggc tggggtgagg   1120
gctagtagga gaaccatgag ttggggcaaa cacagagaac tgaactgaca gcttcagtac   1180
aaggagctct gcttcatcca gacccaagga agggaacctg tgaggttact cgggtaaagc   1240
tgggaggccc aaggtccagg ggacagcctg ggtgtagctt ctacagtgtg acagacacca   1300
agtagagtca gaaggcaaga ccgggctcta acaattggtc actcttgggc aagtcacttt   1360
agctctcaaa ctctactttc tctatcagtg aaatggagtt gatgatgtct gccctccaag   1420
actgtttgga gaataccaac ctagtaagag gcatgaaagg gggtgcaaac agaaaaacta   1480
ggaggaagaa gctgggattg gaatgcaggt ctcttgcggg atgtggtgtg ggaggagaat   1540
gcacaaatgg acagagtggg ggttggggggc tgggaaagag ctaaggacca gggcaggagg   1600
ggattcaaga gactgagtag ggcagctagc tagttcctgg gagctcttcc cttgtcatct   1660
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gaccactgtg tcctgcatca gactaaccag gtccccaggg tgtggggtcc agagcccttg   1780
gacatgaata ctggggcaga accatgcaca tgtggtgaaa taccaaaact ggatgagcct   1840
ttagaaacca ggctccaaaa agtttttattt tacagatggg aagtctgggg ccagggtgaa   1900
ggcacatctt cctcagggcc actcagctgg ggtgcgggga gctcagatct gaaccccaat   1960
cttctgactc tttacctagc cccagaacaa ggtggctgat gaggcagagc tatgccggca   2020
ccgtctggat gtggtcccca agccagggct tgtcctggga ggcgtttttt tgtttgtttt   2080
ttaaaaattg tgctacaggt gagaggttga gaaatggatg caaaccatcg tctgtgttcc   2140
tcttctag tg cag gta ccc ttc tcc aga tgt tgc ttc tca ttt gcg gag   2189
          Met Gln Val Pro Phe Ser Arg Cys Cys Phe Ser Phe Ala Glu
                          30                      35

caa gag att ccc ctg agg gca atc ctg tgt tac aga aat acc agc tcc   2237
Gln Glu Ile Pro Leu Arg Ala Ile Leu Cys Tyr Arg Asn Thr Ser Ser
 40              45              50                      55

atc tgc tcc aat gag ggc tta at gtaagtgatc acctgctcaa tctctcccta   2290
Ile Cys Ser Asn Glu Gly Leu Ile
                60

gagaacagaa ccccgccagc ctggaattac aagagtagac actagatgac agtattttac   2350
tggaataagg tttctaaacc cagagctgcc agcacctggg tgcaagccac acttgggcgc   2410
tagagggagc gctgagcttc ctagcaggtg tgaggaagga tgcatctgtg ctcctgcagt   2470
ggcttgtgtt tcctgaaact ccaaggtgcc aagtattgta tcccagcatt atgagctcag   2530
aggtttaaca aaagcatgag gggttattgt gcactggaaa gagcaaggga accaggatga   2590
gttcctgccc ctggatttgg aacccatagt cttgggtgac cgtggacagg taactccttt   2650
gtactgaatt gtctgtgtat ccttctgtat tccttatctg tgaagggtca taaacatagc   2710
tgcatcacag ggtctttaca aacttaattg gagtagcttt cacataccag tcagtatttt   2770
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gcggggcttg tgcgttgccc acccagtggt ggcttgggtg gctcagcctt ctctcttatt   3370
ctctgttcac ag a ttc aag ctg aag aga ggc aaa gag gcc tgc gcc ttg   3419
               Phe Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu
               65                  70                      75

gac aca gtt gga tgg gtt cag agg cac aga aaa atg ctg agg cac tgc   3467
Asp Thr Val Gly Trp Val Gln Arg His Arg Lys Met Leu Arg His Cys
                80              85                      90

ccg tca aaa aga aaa tgagcagatt tctttccatt gtgggctctg gaaaccacat   3522
Pro Ser Lys Arg Lys
                95
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ggcttcacct gtccccgaaa ctaccagccc tacaccattc cttctgccct gcttttgcta    3582
ggtcacagag gatctgcttg gtcttgataa gctatgttgt tgcactttaa acatttaaat    3642
tatacaatca tcaacccca accctctggg ctcttggatt tcagagtgaa aacttgatgg      3702
cattgag                                                              3709


<210> 37
<211> 673
<212> DNA
<213> Homo sapiens


<220>
<221> CDS
<222> (67)...(450)


<400> 37
gggcaactca ccctcactca gaggtcttct ggttctggaa acaactctag ctcagccttc     60
tccacc atg agc ctc aga ctt gat acc acc cct tcc tgt aac agt gcg       108
       Met Ser Leu Arg Leu Asp Thr Thr Pro Ser Cys Asn Ser Ala
        1               5                  10


aga cca ctt cat gcc ttg cag gtg ctg ctg ctt ctg tca ttg ctg ctg     156
Arg Pro Leu His Ala Leu Gln Val Leu Leu Leu Leu Ser Leu Leu Leu
 15              20                  25                  30


act gct ctg gct tcc tcc acc aaa gga caa act aag aga aac ttg gcg     204
Thr Ala Leu Ala Ser Ser Thr Lys Gly Gln Thr Lys Arg Asn Leu Ala
                 35                  40                  45


aaa ggc aaa gag gaa agt cta gac agt gac ttg tat gct gaa ctc cgc     252
Lys Gly Lys Glu Glu Ser Leu Asp Ser Asp Leu Tyr Ala Glu Leu Arg
             50                  55                  60


tgc atg tgt ata aag aca acc tct gga att cat ccc aaa aac atc caa     300
Cys Met Cys Ile Lys Thr Thr Ser Gly Ile His Pro Lys Asn Ile Gln
             65                  70                  75


agt ttg gaa gtg atc ggg aaa gga acc cat tgc aac caa gtc gaa gtg     348
Ser Leu Glu Val Ile Gly Lys Gly Thr His Cys Asn Gln Val Glu Val
         80                  85                  90


ata gcc aca ctg aag gat ggg agg aaa atc tgc ctg gac cca gat gct     396
Ile Ala Thr Leu Lys Asp Gly Arg Lys Ile Cys Leu Asp Pro Asp Ala
 95                  100                 105                 110


ccc aga atc aag aaa att gta cag aaa aaa ttg gca ggt gat gaa tct     444
Pro Arg Ile Lys Lys Ile Val Gln Lys Lys Leu Ala Gly Asp Glu Ser
                 115                 120                 125


gct gat taatttgttc tgtttctgcc aaacttcttt aactcccagg aagggtagaa     500
Ala Asp


ttttgaaacc ttgatttct agagttctca tttattcagg atacctattc ttactgtatt    560
aaaatttgga tatgtgtttc attctgtctc aaaaatcaca ttttattctg agaaggttgg   620
ttaaaagatg gcagaaagaa gatgaaaata ataagcctg gtttcaaccc tct            673


<210> 38
<211> 12
<212> PRT
<213> Homo sapiens


<400> 38
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Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
 1           5                   10


<210> 39
<211> 2545
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (40)...(414)

<400> 39
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                                            Met Lys Lys Ser Gly
                                             1               5


gtt ctt ttc ctc ttg ggc atc atc ttg ctg gtt ctg att gga gtg caa        102
Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val Leu Ile Gly Val Gln
                10                  15                  20


gga acc cca gta gtg aga aag ggt cgc tgt tcc tgc atc agc acc aac        150
Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser Cys Ile Ser Thr Asn
            25                  30                  35


caa ggg act atc cac cta caa tcc ttg aaa gac ctt aaa caa ttt gcc        198
Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp Leu Lys Gln Phe Ala
        40                  45                  50


cca agc cct tcc tgc gag aaa att gaa atc att gct aca ctg aag aat        246
Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile Ala Thr Leu Lys Asn
    55                  60                  65


gga gtt caa aca tgt cta aac cca gat tca gca gat gtg aag gaa ctg        294
Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala Asp Val Lys Glu Leu
70                  75                  80                  85


att aaa aag tgg gag aaa cag gtc agc caa aag aaa aag caa aag aat        342
Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys Lys Lys Gln Lys Asn
                90                  95                  100


ggg aaa aaa cat caa aaa aag aaa gtt ctg aaa gtt cga aaa tct caa        390
Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys Val Arg Lys Ser Gln
            105                 110                 115


cgt tct cgt caa aag aag act aca taagagacca cttcaccaat aagtattctg       444
Arg Ser Arg Gln Lys Lys Thr Thr
            120                 125


tgttaaaaat gttctatttt aattataccg ctatcattcc aaaggaggat ggcatataat       504
acaaaggctt attaatttga ctagaaaatt taaaacatta ctctgaaatt gtaactaaag       564
ttagaaagtt gattttaaga atccaaacgt taagaattgt taaaggctat gattgtcttt       624
gttcttctac cacccaccag ttgaatttca tcatgcttaa ggccatgatt ttagcaatac       684
ccatgtctac acagatgttc acccaaccac atcccactca caacagctgc ctggaagagc       744
agccctaggc ttccacgtac tgcagcctcc agagagtatc tgaggcacat gtcagcaagt       804
cctaagcctg ttagcatgct ggtgagccaa gcagtttgaa attgagctgg acctcaccaa       864
gctgctgtgg ccatcaacct ctgtatttga atcagcctac aggcctcaca cacaatgtgt       924
ctgagagatt catgctgatt gttattgggt atcaccactg agatcacca gtgtgtggct       984
ttcagagcct cctttctggc tttggaagcc atgtgattcc atcttgcccg ctcaggctga      1044
ccactttatt tcttttttgtt cccctttgct tcattcaagt cagctcttct ccatcctacc     1104
acaatgcagt gcctttcttc tctccagtgc acctgtcata tgctctgatt tatctgagtc      1164
aactcctttc tcatcttgtc cccaacaccc cacagaagtg ctttcttctc ccaattcatc      1224
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19

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ctcactcagt ccagcttagt tcaagtcctg cctcttaaat aaaccttttt ggacacacaa   1284
attatcttaa aactcctgtt tcacttggtt cagtaccaca tgggtgaaca ctcaatggtt ·  1344
aactaattct tgggtgttta tcctatctct ccaaccagat tgtcagctcc ttgagggcaa   1404
gagccacagt atatttccct gtttcttcca cagtgcctaa taatactgtg gaactaggtt   1464
ttaataattt tttaattgat gttgttatgg gcaggatggc aaccagacca ttgtctcaga   1524
gcaggtgctg gctctttcct ggctactcca tgttggctag cctctggtaa cctcttactt   1584
attatcttca ggacactcac tacagggacc agggatgatg caacatcctt gtctttttat   1644
gacaggatgt ttgctcagct tctccaacaa taagaagcac gtggtaaaac acttgcggat   1704
attctggact gttttttaaaa aatatacagt ttaccgaaaa tcatataatc ttacaatgaa   1764
aaggactttta tagatcagcc agtgaccaac cttttcccaa ccatacaaaa attccttttc   1824
ccgaaggaaa agggctttct caataagcct cagctttcta agatctaaca agatagccac   1884
cgagatcctt atcgaaactc attttaggca aatatgagtt ttattgtccg tttacttgtt   1944
tcagagtttg tattgtgatt atcaattacc acaccatctc ccatgaagaa agggaacggt   2004
gaagtactaa gcgctagagg aagcagccaa gtcggttagt ggaagcatga ttggtgccca   2064
gttagcctct gcaggatgtg gaaacctcct tccaggggag gttcagtgaa ttgtgtagga   2124
gaggttgtct gtggccagaa tttaaaccta tactcacttt cccaaattga atcactgctc   2184
acactgctga tgatttagag tgctgtccgg tggagatccc acccgaacgt cttatctaat   2244
catgaaactc cctagttcct tcatgtaact tccctgaaaa atctaagtgt ttcataaatt   2304
tgagagtctg tgacccactt accttgcatc tcacaggtag acagtatata actaacaacc   2364
aaagactaca tattgtcact gacacacacg ttataatcat ttatcatata tatacataca   2424
tgcatacact ctcaaagcaa ataatttttc acttcaaaac agtattgact tgtataccttt  2484
gtaatttgaa atattttctt tgttaaaata gaatggtatc aataaataga ccattaatca   2544
g                                                                   2545

<210> 40
<211> 12
<212> PRT
<213> Homo sapiens

<400> 40
Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val Gln
1               5                   10

<210> 41
<211> 12
<212> PRT
<213> Homo sapiens

<400> 41
Glu Ile Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys
1               5                   10

<210> 42
<211> 12
<212> PRT
<213> Homo sapiens

<400> 42
Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln
1               5                   10

<210> 43
<211> 12
<212> PRT
<213> Homo sapiens

<400> 43
Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln
1               5                   10

<210> 44
<211> 12
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<212> PRT
<213> Homo sapiens

<400> 44
Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln
1   5   10

<210> 45
<211> 125
<212> PRT
<213> Homo sapiens

<400> 45
Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val
1   5   10   15
Leu Ile Gly Val Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser
            20   25   30
Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp
            35   40   45
Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile
        50   55   60
Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala
65   70   75   80
Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys
                85   90   95
Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
            100   105   110
Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
            115   120   125

<210> 46
<211> 128
<212> PRT
<213> Homo sapiens

<400> 46
Met Ser Leu Arg Leu Asp Thr Thr Pro Ser Cys Asn Ser Ala Arg Pro
1   5   10   15
Leu His Ala Leu Gln Val Leu Leu Leu Leu Ser Leu Leu Leu Thr Ala
            20   25   30
Leu Ala Ser Ser Thr Lys Gly Gln Thr Lys Arg Asn Leu Ala Lys Gly
            35   40   45
Lys Glu Glu Ser Leu Asp Ser Asp Leu Tyr Ala Glu Leu Arg Cys Met
        50   55   60
Cys Ile Lys Thr Thr Ser Gly Ile His Pro Lys Asn Ile Gln Ser Leu
65   70   75   80
Glu Val Ile Gly Lys Gly Thr His Cys Asn Gln Val Glu Val Ile Ala
                85   90   95
Thr Leu Lys Asp Gly Arg Lys Ile Cys Leu Asp Pro Asp Ala Pro Arg
            100   105   110
Ile Lys Lys Ile Val Gln Lys Lys Leu Ala Gly Asp Glu Ser Ala Asp
        115   120   125

<210> 47
<211> 96
<212> PRT
<213> Homo sapiens

<400> 47
Met Gln Ile Ile Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met
1   5   10   15

21

Trp Pro Glu Asp Val Asp Ser Lys Ser Met Gln Val Pro Phe Ser Arg
        20   25   30
Cys Cys Phe Ser Phe Ala Glu Gln Glu Ile Pro Leu Arg Ala Ile Leu
        35   40   45
Cys Tyr Arg Asn Thr Ser Ser Ile Cys Ser Asn Glu Gly Leu Ile Phe
    50   55   60
Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu Asp Thr Val Gly Trp
65   70   75   80
Val Gln Arg His Arg Lys Met Leu Arg His Cys Pro Ser Lys Arg Lys
            85   90   95

<210> 48
<211> 93
<212> PRT
<213> Homo sapiens

<400> 48
Met Lys Ile Ser Val Ala Ala Ile Pro Phe Phe Leu Leu Ile Thr Ile
1   5   10   15
Ala Leu Gly Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro
        20   25   30
Ser Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg
        35   40   45
Ile Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile
    50   55   60
Val Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp
65   70   75   80
Lys Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn
            85   90

<210> 49
<211> 93
<212> PRT
<213> Homo sapiens

<400> 49
Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
1   5   10   15
Leu Cys Asn Gln Val Leu Ser Ala Pro Leu Ala Ala Asp Thr Pro Thr
        20   25   30
Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile
        35   40   45
Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Ser Val Ile
    50   55   60
Phe Leu Thr Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu
65   70   75   80
Trp Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
            85   90

<210> 50
<211> 98
<212> PRT
<213> Homo sapiens

<400> 50
Met Lys Val Ser Ala Val Leu Leu Cys Leu Leu Leu Met Thr Ala Ala
1   5   10   15
Phe Asn Pro Gln Gly Leu Ala Gln Pro Asp Ala Leu Asn Val Pro Ser
        20   25   30
Thr Cys Cys Phe Thr Phe Ser Ser Lys Lys Ile Ser Leu Gln Arg Leu
        35   40   45

22

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Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val Ile
    50              55              60
Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys
65              70              75              80
Trp Val Gln Asn Tyr Met Lys His Leu Gly Arg Lys Ala His Thr Leu
                85              90              95
Lys Thr


<210> 51
<211> 839
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (54)...(344)

<400> 51
caacccagaa accaccacct ctcacgccaa agctcacacc ttcagcctcc aac atg          56
                                                            Met
                                                            1


aag gtc tcc gca gca ctt ctg tgg ctg ctg ctc ata gca gct gcc ttc        104
Lys Val Ser Ala Ala Leu Leu Trp Leu Leu Leu Ile Ala Ala Ala Phe
            5                   10                  15

agc ccc cag ggg ctc gct ggg cca gct tct gtc cca acc acc tgc tgc        152
Ser Pro Gln Gly Leu Ala Gly Pro Ala Ser Val Pro Thr Thr Cys Cys
            20                  25                  30

ttt aac ctg gcc aat agg aag ata ccc ctt cag cga cta gag agc tac        200
Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr
        35                  40                  45

agg aga atc acc agt ggc aaa tgt ccc cag aaa gct gtg atc ttc aag        248
Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys
    50                  55                  60                  65

acc aaa ctg gcc aag gat atc tgt gcc gac ccc aag aag aag tgg gtg        296
Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val
                70                  75                  80

cag gat tcc atg aag tat ctg gac caa aaa tct cca act cca aag cca        344
Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro
                85                  90                  95


taaataatca ccattttga aaccaaacca gagcctgagt gttgcctaat ttgttttccc        404
ttcttacaat gcattctgag gtaacctcat tatcagtcca aagggcatgg gttttattat        464
atatatatat atatatttt tttaaaaaa aaacgtattg catttaattt attgaggctt         524
taaaacttat cctccatgaa tatcagttat ttttaaactg taaagctttg tgcagattct        584
ttaccccctg ggagccccaa ttcgatcccc tgtcacgtgt gggcaatgtt cccctctcc         644
tctcttcctc cctggaatct tgtaaaggtc ctggcaaaga tgatcagtat gaaaatgtca        704
ttgttcttgt gaacccaaag tgtgactcat taaatggaag taatgttgtt ttaggaatac        764
ataaagtatg tgcatatttt attatagtca ctagttgtaa ttttttgtg ggaaatccac         824
actgagctga ggggg                                                         839

<210> 52
<211> 114
<212> PRT
<213> Homo sapiens
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61

23

<400> 52
Met Ser Leu Leu Ser Ser Arg Ala Ala Arg Val Pro Gly Pro Ser Ser
1   5   10   15
Ser Leu Cys Ala Leu Leu Val Leu Leu Leu Leu Thr Gln Pro Gly
            20   25   30
Pro Ile Ala Ser Ala Gly Pro Ala Ala Ala Val Leu Arg Glu Leu Arg
        35   40   45
Cys Val Cys Leu Gln Thr Thr Gln Gly Val His Pro Lys Met Ile Ser
    50   55   60
Asn Leu Gln Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu Val
65   70   75   80
Val Ala Ser Leu Lys Asn Gly Lys Glu Ile Cys Leu Asp Pro Glu Ala
                85   90   95
Pro Phe Leu Lys Lys Val Ile Gln Lys Ile Leu Asp Gly Gly Asn Lys
            100   105   110
Glu Asn

<210> 53
<211> 107
<212> PRT
<213> Homo sapiens

<400> 53
Met Ala Arg Ala Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
1   5   10   15
Arg Val Ala Leu Leu Leu Leu Leu Leu Val Ala Ala Ser Arg Arg Ala
            20   25   30
Ala Gly Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
        35   40   45
Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser
    50   55   60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65   70   75   80
Gly Gln Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile
                85   90   95
Ile Glu Lys Met Leu Lys Asn Gly Lys Ser Asn
            100   105

<210> 54
<211> 98
<212> PRT
<213> Homo sapiens

<400> 54
Met Asn Pro Ser Ala Ala Val Ile Phe Cys Leu Ile Leu Leu Gly Leu
1   5   10   15
Ser Gly Thr Gln Gly Ile Pro Leu Ala Arg Thr Val Arg Cys Asn Cys
            20   25   30
Ile His Ile Asp Asp Gly Pro Val Arg Met Arg Ala Ile Gly Lys Leu
        35   40   45
Glu Ile Ile Pro Ala Ser Leu Ser Cys Pro Arg Val Glu Ile Ile Ala
    50   55   60
Thr Met Lys Lys Asn Asp Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys
65   70   75   80
Thr Ile Lys Asn Leu Met Lys Ala Phe Ser Gln Lys Arg Ser Lys Arg
                85   90   95
Ala Pro

<210> 55
<211> 1041

24

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (18)...(338)

<400> 55
cccgcctgct gagcccc atg gcc cgc gct gct ctc tcc gcc gcc ccc agc   50
                    Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser
                     1   5   10

aat ccc cgg ctc ctg cga gtg gca ctg ctg ctc ctg ctc ctg gta gcc   98
Asn Pro Arg Leu Leu Arg Val Ala Leu Leu Leu Leu Leu Leu Val Ala
         15   20   25

gct ggc cgg cgc gca gca gga gcg tcc gtg gcc act gaa ctg cgc tgc   146
Ala Gly Arg Arg Ala Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys
         30   35   40

cag tgc ttg cag acc ctg cag gga att cac ccc aag aac atc caa agt   194
Gln Cys Leu Gln Thr Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser
     45   50   55

gtg aac gtg aag tcc ccc gga ccc cac tgc gcc caa acc gaa gtc ata   242
Val Asn Val Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile
 60   65   70   75

gcc aca ctc aag aat ggg cgg aaa gct tgc ctc aat cct gca tcc ccc   290
Ala Thr Leu Lys Asn Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro
                 80   85   90

ata gtt aag aaa atc atc gaa aag atg ctg aac agt gac aaa tcc aac   338
Ile Val Lys Lys Ile Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
             95   100   105

tgaccagaag ggaggaggaa gctcactggt ggctgttcct gaaggaggcc ctgcccttat   398
aggaacagaa gaggaaagag agacacagct gcagaggcca cctggattgt gcctaatgtg   458
tttgagcatc gcttaggaga agtcttctat ttatttattt attcattagt tttgaagatt   518
ctatgttaat attttaggtg taaaataatt aagggtatga ttaactctac ctgcacactg   578
tcctattata ttcattcttt ttgaaatgtc aaccccaagt tagttcaatc tggattcata   638
tttaatttga aggtagaatg ttttcaaatg ttctccagtc attatgttaa tatttctgag   698
gagcctgcaa catgccagcc actgtgatag aggctggcgg atccaagcaa atggccaatg   758
agatcattgt gaaggcaggg gaatgtatgt gcacatctgt tttgtaactg tttagatgaa   818
tgtcagttgt tatttattga aatgatttca cagtgtgtgg tcaacatttc tcatgttgaa   878
actttaagaa ctaaaatgtt ctaaatatcc cttggacatt ttatgtcttt cttgtaaggc   938
atactgcctt gtttaatggt agttttacag tgtttctggc ttagaacaaa ggggcttaat   998
tattgatgtt ttcatagaga atataaaaat aaagcactta tag   1041

<210> 56
<211> 93
<212> PRT
<213> Homo sapiens

<400> 56
Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
 1   5   10   15
Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
             20   25   30
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
             35   40   45

25

```
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
    50              55              60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65              70              75              80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
            85              90


<210> 57
<211> 107
<212> PRT
<213> Homo sapiens


<400> 57
Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
  1           5               10              15
Arg Val Ala Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
            20              25              30
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
        35              40              45
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
    50              55              60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65              70              75              80
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
            85              90              95
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
            100             105


<210> 58
<211> 1560
<212> DNA
<213> Homo sapiens


<220>
<221> CDS
<222> (102)...(398)


<400> 58
ctccataagg cacaaacttt cagagacagc agagcacaca agcttctagg acaagagcca      60
ggaagaaacc accggaagga accatctcac tgtgtgtaaa c atg act tcc aag ctg     116
                                            Met Thr Ser Lys Leu
                                              1               5


gcc gtg gct ctc ttg gca gcc ttc ctg att tct gca gct ctg tgt gaa     164
Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser Ala Ala Leu Cys Glu
                10              15              20


ggt gca gtt ttg cca agg agt gct aaa gaa ctt aga tgt cag tgc ata     212
Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile
            25              30              35


aag aca tac tcc aaa cct ttc cac ccc aaa ttt atc aaa gaa ctg aga     260
Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg
        40              45              50


gtg att gag agt gga cca cac tgc gcc aac aca gaa att att gta aag     308
Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys
    55              60              65


ctt tct gat gga aga gag ctc tgt ctg gac ccc aag gaa aac tgg gtg     356
Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val
70              75              80              85
```

26

```
cag agg gtt gtg gag aag ttt ttg aag agg gct gag aat tca                398
Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser
              90                  95


taaaaaaatt cattctctgt ggtatccaag aatcagtgaa gatgccagtg aaacttcaag     458
caaatctact tcaacacttc atgtattgtg tgggtctgtt gtagggttgc cagatgcaat     518
acaagattcc tggttaaatt tgaatttcag taaacaatga atagtttttc attgtaccat     578
gaaatatcca gaacatactt atatgtaaag tattatttat ttgaatctac aaaaaacaac     638
aaataatttt taaatataag gattttccta gatattgcac gggagaatat acaaatagca     698
aaattgggcc aagggccaag agaatatccg aactttaatt tcaggaattg aatgggtttg     758
ctagaatgtg atatttgaag catcacataa aaatgatggg acaataaatt ttgccataaa     818
gtcaaattta gctggaaatc ctggattttt ttctgttaaa tctggcaacc ctagtctgct     878
agccaggatc cacaagtcct tgttccactg tgccttggtt tctcctttat ttctaagtgg     938
aaaaagtatt agccaccatc ttacctcaca gtgatgttgt gaggacatgt ggaagcactt     998
taagtttttt catcataaca taaattattt tcaagtgtaa cttattaacc tatttattat    1058
ttatgtattt atttaagcat caaatatttg tgcaagaatt tggaaaaata gaagatgaat    1118
cattgattga atagttataa agatgttata gtaaatttat tttatttttag atattaaatg    1178
atgttttatt agataaattt caatcagggt ttttagatta aacaaacaaa caattgggta    1238
cccagttaaa tttttcatttc agatatacaa caaataattt tttagtataa gtacattatt    1298
gtttatctga aattttaatt gaactaacaa tcctagtttg atactcccag tcttgtcatt    1358
gccagctgtg ttggtagtgc tgtgttgaat tacggaataa tgagttagaa ctattaaaac    1418
agccaaaact ccacagtcaa tattagtaat ttcttgctgg ttgaaacttg tttattatgt    1478
acaaatagat tcttataata ttatttaaat gactgcattt ttaaatacaa ggctttatat    1538
ttttaacttt aaaaaaaacc gg                                            1560


<210> 59
<211> 15
<212> PRT
<213> Homo sapiens


<400> 59
Asn Leu Gln Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu
1               5                   10                  15


<210> 60
<211> 14
<212> PRT
<213> Homo sapiens


<400> 60
Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala
1               5                   10


<210> 61
<211> 15
<212> PRT
<213> Homo sapiens


<400> 61
Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val
1               5                   10                  15


<210> 62
<211> 15
<212> PRT
<213> Homo sapiens


<400> 62
Glu Ser Tyr Arg Arg Ile Thr Asn Ile Gln Cys Pro Lys Glu Ala
1               5                   10                  15
```

<210> 63
<211> 15
<212> PRT
<213> Homo sapiens

<400> 63
Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala
1   5   10   15

<210> 64
<211> 15
<212> PRT
<213> Homo sapiens

<400> 64
Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val
1   5   10   15

<210> 65
<211> 12
<212> PRT
<213> Homo sapiens

<400> 65
Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln
1   5   10

<210> 66
<211> 12
<212> PRT
<213> Homo sapiens

<400> 66
Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln
1   5   10

<210> 67
<211> 12
<212> PRT
<213> Homo sapiens

<400> 67
Glu Ile Cys Ala Asp Pro Lys Glu Arg Trp Val Arg
1   5   10

<210> 68
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)...(16)
<223> Xaa = any amino acid

<400> 68
Met Ile Cys Ala Asp Pro Lys Xaa Ala Ala Xaa Ala Ala Trp Val Gln
1   5   10   15

<210> 69
<211> 15
<212> PRT

28

<213> Homo sapiens

<400> 69
Ser Val Asn Val Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu
1   5   10   15

<210> 70
<211> 15
<212> PRT
<213> Homo sapiens

<400> 70
Ser Val Lys Val Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu
1   5   10   15

<210> 71
<211> 15
<212> PRT
<213> Homo sapiens

<400> 71
Ser Val Asn Val Arg Ser Pro Gly Pro His Cys Ala Gln Thr Glu
1   5   10   15

<210> 72
<211> 12
<212> PRT
<213> Homo sapiens

<400> 72
Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys
1   5   10

<210> 73
<211> 12
<212> PRT
<213> Homo sapiens

<400> 73
Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys
1   5   10

<210> 74
<211> 12
<212> PRT
<213> Homo sapiens

<400> 74
Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln
1   5   10

<210> 75
<211> 12
<212> PRT
<213> Homo sapiens

<400> 75
Lys Ser Tyr Lys Ile Ile Thr Ser Ser Lys Cys Pro
1   5   10

<210> 76
<211> 661

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (32)...(331)

<400> 76
tcaaactgaa gctcgcactc tcgcctccag c atg aaa gtc tct gcc gcc ctt   52
                                    Met Lys Val Ser Ala Ala Leu
                                     1   5

ctg tgc ctg ctg ctc ata gca gcc acc ttc att ccc caa ggg ctc gct   100
Leu Cys Leu Leu Leu Ile Ala Ala Thr Phe Ile Pro Gln Gly Leu Ala
         10   15   20

cag cca gat gca atc aat gcc cca gtc acc tgc tgc tat aac ttc acc   148
Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe Thr
     25   30   35

aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc acc   196
Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile Thr
 40   45   50   55

agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg gcc   244
Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val Ala
                 60   65   70

aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc atg   292
Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Met
             75   80   85

gac cac ctg gac aag caa acc caa act ccg aag act tga acactcactc   341
Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr *
             90   95

cacaacccaa gaatctgcag ctaacttatt ttcccctagc tttccccaga catcctgttt   401
tattttatta taatgaattt tgtttgttga tgtgaaacat tatgccttaa gtaatgttaa   461
ttcttattta agttattgat gttttaagtt tatctttcat ggtactagtg ttttttagat   521
acagagactt ggggaaattg cttttcctct tgaaccacag ttctacccct gggatgtttt   581
gagggtcttt gcaagaatca ttttttttaac attccaatgc atttaataca aagaattgct   641
aaaatattat tgtggaaatg   661

<210> 77
<211> 1847
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (80)...(346)

<400> 77
tctccgtcag ccgcattgcc cgctcggcgt ccggcccccg acccgtgctc gtccgcccgc   60
ccgcccgccc gcccgcgcc atg aac gcc aag gtc gtg gtc gtg ctg gtc ctc   112
                     Met Asn Ala Lys Val Val Val Val Leu Val Leu
                      1   5   10

gtg ctg acc gcg ctc tgc ctc agc gac ggg aag ccc gtc agc ctg agc   160
Val Leu Thr Ala Leu Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser
             15   20   25

                                    30

```
tac aga tgc cca tgc cga ttc ttc gaa agc cat gtt gcc aga gcc aac      208
Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn
         30                  35                  40

gtc aag cat ctc aaa att ctc aac act cca aac tgt gcc ctt cag att      256
Val Lys His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile
         45                  50                  55

gta gcc cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aag      304
Val Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
     60                  65                  70                  75

cta aag tgg att cag gag tac ctg gag aaa gct tta aac aag            346
Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys
                 80                  85

taagcacaac agccaaaaag gactttccgc tagacccact cgaggaaaac taaaaccttg   406
tgagagatga aagggcaaag acgtggggga gggggcctta accatgagga ccaggtgtgt   466
gtgtggggtg ggcacattga tctgggatcg ggcctgaggt ttgcagcatt tagaccctgc   526
atttatagca tacggtatga tattgcagct tatattcatc catgccctgt acctgtgcac   586
gttggaactt ttattactgg ggtttttcta agaaagaaat tgtattatca acagcatttt   646
caagcagtta gttccttcat gatcatcaca atcatcatca ttctcattct cattttttaa   706
atcaacgagt acttcaagat ctgaatttgg cttgtttgga gcatctcctc tgctcccctg   766
gggagtctgg gcacagtcag gtggtggctt aacaggagc tggaaaaagt gtcctttctt    826
cagacactga ggctcccgca gcagcgcccc tcccaagagg aaggcctctg tggcactcag   886
ataccgactg gggctggggc gccgccactg ccttcacctc ctctttcaaa cctcagtgat   946
tggctctgtg ggctccatgt agaagccact attactggga ctgtctcaga gacccctctc  1006
ccagctattc ctactctctc cccgactccg agagcatgct taatcttgct tctgcttctc  1066
atttctgtag cctgatcagc gccgcaccag ccgggaagag ggtgattgct ggggctcgtg  1126
ccctgcatcc ctctcctccc agggcctgcc ccacagctcg ggccctctgt gagatccgtc  1186
tttggcctcc tccagaatgg agctggccct ctcctgggga tgtgtaatgg tcccccctgct 1246
tacccgcaaa agacaagtct ttacagaatc aaatgcaatt ttaaatctga gagctcgctt  1306
gagtgactgg gtttgtgatt gcctctgaag cctatgtatg ccatggaggc actaacaaac  1366
tctgaggttt ccgaaatcag aagcgaaaaa atcagtgaat aaaccatcat cttgccacta  1426
cccccctcctg aagccacagc aggggttcag gttccaatca gaactgttgg caaggtgaca  1486
tttccatgca tagatgcgat ccacagaagg tcctggtggt atttgtaact ttttgcaagg  1546
cattttttta tatatatttt tgtgcacatt ttttttacg attctttaga aaacaaatgt   1606
atttcaaaat atatttatag tcgaacaagt catatatatg aatgagagcc atatgaatgt  1666
cagtagttta tacttctcta ttatctcaaa ctactggcaa tttgtaaaga aatatatatg  1726
atatataaat gtgattgcag cttttcaatg ttagccacag tgtattttt cacttgtact   1786
aaaattgtat caaatgtgac attatatgca ctagcaataa aatgctaatt gtttcatggt  1846
a                                                                   1847
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<210> 78
<211> 1160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (27)...(299)

<400> 78
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cctccgacag cctctccaca ggtacc atg aag gtc tcc gcg gca cgc ctc gct    53
                              Met Lys Val Ser Ala Ala Arg Leu Ala
                               1               5


gtc atc ctc att gct act gcc ctc tgc gct cct gca tct gcc tcc cca    101
Val Ile Leu Ile Ala Thr Ala Leu Cys Ala Pro Ala Ser Ala Ser Pro
     10                  15                  20                  25
```

31

```
tat tcc tcg gac acc aca ccc tgc tgc ttt gcc tac att gcc cgc cca      149
Tyr Ser Ser Asp Thr Thr Pro Cys Cys Phe Ala Tyr Ile Ala Arg Pro
                30              35                  40

ctg ccc cgt gcc cac atc aag gag tat ttc tac acc agt ggc aag tgc      197
Leu Pro Arg Ala His Ile Lys Glu Tyr Phe Tyr Thr Ser Gly Lys Cys
                45              50                  55

tcc aac cca gca gtc gtc ttt gtc acc cga aag aac cgc caa gtg tgt      245
Ser Asn Pro Ala Val Val Phe Val Thr Arg Lys Asn Arg Gln Val Cys
            60              65                  70

gcc aac cca gag aag aaa tgg gtt cgg gag tac atc aac tct ttg gag      293
Ala Asn Pro Glu Lys Lys Trp Val Arg Glu Tyr Ile Asn Ser Leu Glu
        75              80                  85

atg agc taggatggag agtccttgaa cctgaactta cacaaatttg cctgtttctg      349
Met Ser
 90

cttgctcttg tcctagcttg ggaggcttcc cctcactatc ctaccccacc cgctccttga      409
agggcccaga ttctgaccac gacgagcagc agttacaaaa accttcccca ggctggacgt      469
ggtggctcag ccttgtaatc ccagcacttt gggaggccaa ggtgggtgga tcacttgagg      529
tcaggagttc gagacagcct ggccaacatg atgaaacccc atgtgtacta aaaatacaaa      589
aaattagccg ggcgtggtag cgggcgcctg tagtcccagc tactcgggag gctgaggcag      649
gagaatggcg tgaacccggg agcggagctt gcagtgagcc gagatcgcgc cactgcactc      709
cagcctgggc gacagagcga gactccgtct caaaaaaaaa aaaaaaaaaa aaaaaaatac      769
aaaaattagc cgcgtggtgg cccacgcctg taatcccagc tactcgggag gctaaggcag      829
gaaaattgtt tgaacccagg aggtggaggc tgcagtgagc tgagattgtg ccacttcact      889
ccagcctggg tgacaaagtg agactccgtc acaacaacaa caacaaaaag cttccccaac      949
taaagcctag aagagcttct gaggcgctgc tttgtcaaaa ggaagtctct aggttctgag      1009
ctctggcttt gccttggctt tgcaagggct ctgtgacaag gaaggaagtc agcatgcctc      1069
tagaggcaag gaagggagga acactgcact cttaagcttc cgccgtctca accccctcaca      1129
ggagcttact ggcaaacatg aaaaatcggg g                                     1160

<210> 79
<211> 696
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (109)...(384)

<400> 79
ttcccccccc cccccccccc ccccgcccga gcacaggaca cagctgggtt ctgaagcttc      60
tgagttctgc agcctcacct ctgagaaaac ctcttttcca ccaatacc atg aag ctc     117
                                                         Met Lys Leu
                                                          1

tgc gtg act gtc ctg tct ctc ctc atg cta gta gct gcc ttc tgc tct      165
Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala Phe Cys Ser
 5                  10                  15

cca gcg ctc tca gca cca atg ggc tca gac cct ccc acc gcc tgc tgc      213
Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys Cys
 20              25                  30                  35

ttt tct tac acc gcg agg aag ctt cct cgc aac ttt gtg gta gat tac      261
Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp Tyr
            40                  45                  50
```

32

```
tat gag acc agc agc ctc tgc tcc cag cca gct gtg gta ttc caa acc     309
Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln Thr
            55                  60                  65

aaa aga agc aag caa gtc tgt gct gat ccc agt gaa tcc tgg gtc cag     357
Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln
        70                  75                  80

gag tac gtg tat gac ctg gaa ctg aac tgagctgctc agagacagga           404
Glu Tyr Val Tyr Asp Leu Glu Leu Asn
    85                  90

agtcttcagg gaaggtcacc tgagcccgga tgcttctcca tgagacacat ctcctccata   464
ctcaggactc ctctccgcag ttcctgtccc ttctcttaat ttaatctttt ttatgtgccg   524
tgttattgta ttaggtgtca tttccattat ttatattagt ttagccaaag gataagtgtc   584
ctatggggat ggtccactgt cactgtttct ctgctgttgc aaatacatgg ataacacatt   644
tgattctgtg tgttttccat aataaaactt taaaataaaa tgcagacagt ta           696


<210> 80
<211> 2738
<212> DNA
<213> Homo sapiens


<220>
<221> CDS
<222> (123)...(353)


<400> 80
gaacaaccca gaaaccttca cctctcatgc tgaagctcac acccttgccc tccaagatga     60
aggtttctgc agcgcttctg tgcctgctgc tcatggcagc cactttcagc cctcagggac    120
tt gct cag cca gat tca gtt tcc att cca atc acc tgc tgc ttt aac       167
   Ala Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn
   1               5                   10                  15

gtg atc aat agg aaa att cct atc cag agg ctg gag agc tac aca aga     215
Val Ile Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg
            20                  25                  30

atc acc aac atc caa tgt ccc aag gaa gct gtg atc ttc aag acc caa     263
Ile Thr Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Gln
            35                  40                  45

cgg ggc aag gag gtc tgt gct gac ccc aag gag aga tgg gtc agg gat     311
Arg Gly Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp
        50                  55                  60

tcc atg aag cat ctg gac caa ata ttt caa aat ctg aag cca             353
Ser Met Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
    65                  70                  75


tgagccttca tacatggact gagagtcaga gcttgaagaa aagcttattt attttcccca   413
acctccccca ggtgcagtgt gacattattt tattataaca tccacaaaga gattattttt   473
aaataattta aagcataata tttcttaaaa agtatttaat tatatttaag ttgttgatgt   533
tttaactcta tctgtcatac atcctagtga atgtaaaatg caaaatcctg gtgatgtgtt   593
ttttgttttt gttttcctgt gagctcaact aagttcacgg caaaatgtca ttgttctccc   653
tcctacctgt ctgtagtgtt gtggggtcct cccatggatc atcaaggtga aacactttgg   713
tattctttgg caatcagtgc tcctgtaagt caaatgtgtg ctttgtactg ctgttgttga   773
aattgatgtt actgtatata actatggaat tttgaaaaaa aatttcaaaa agaaaaaaat   833
atatataatt taaaactaag aaaaaaaaaa aaaaaaaaa aaaaaggttt ctattgactt     893
gggttaatcg tgtgaccgcg gtggctggca cgaaattgac caaccctggg gttagtatag   953
cttagttaaa ctttcgttta ttgctaaagg ttaatcactg ctgtttcccg tggggtgtg   1013
gctaggctaa gcgttttgag ctgcattgct gcgtgcttga tgcttgtccc ttttgatcgt  1073
```

33

```
ggtgatttag agggtgaact cactggaatg gggatgcttg catgtgtaat cttactaaga   1133
gctaatagaa aggctaggac caaaccagaa acctccaatt ctcatgtgga agcccatgcc   1193
ctcaccctcc aacatgaaag cctctgcagc acttctgtgt ctgctgctca cagcagctgc   1253
tttcagcccc caggggcttg ctcagccagt tgggattaat acttcaacta cctgctgcta   1313
cagatttatc aataagaaaa tccctaagca gaggctggag agctacagaa ggaccaccag   1373
tagccactgt ccccgggaag ctgtaatctt caagaccaaa ctggacaagg agatctgtgc   1433
tgaccccaca cagaagtggg tccaggactt tatgaagcac ctggacaaga aaacccaaac   1493
tccaaagctt tgaacattca tgactgaact gaaaacaagc catgacttga gaaacaaata   1553
atttgtatac cctgtccttt ctcagagtgg ttctgagatt attttaatct aattctaagg   1613
aatatgagct ttatgtaata atgtgaatca tggttttтct tagtagattt taaaagttat   1673
taatatttta atttaatctt ccatggattt tggtgggttt tgaacataaa gccttggatg   1733
tatatgtcat ctcagtgctg taaaaactgt gggatgctcc tcccttctct acctcatggg   1793
ggtattgtat aagtccttgc aagaatcagt gcaaagattt gctttaattg ttaagatatg   1853
atgtccctat ggaagcatat tgttattata taattacata tttgcatatg tatgactccc   1913
aaattttcac ataaaataga ttтttgtata acaaaaaaaa aaaaaaaaa aaggacacgg   1973
gcagcagaca gtggtcagtc ctttcttggc tctgctgaca ctcgagccca cattccgtca   2033
cctgctcaga atcatgcagg tctccactgc tgcccttgct gtcctcctct gcaccatggc   2093
tctctgcaac cagttctctg catcacttgc tgctgacacg ccgaccgcct gctgcttcag   2153
ctacacctcc cggcagattc cacagaattt catagctgac tactttgaga cgagcagcca   2213
gtgctccaag cccggtgtca tcttcctaac caagcgaagc cggcaggtct gtgctgaccc   2273
cagtgaggag tgggtccaga aatatgtcag cgacctggag ctgagtgcct gaggggtcca   2333
gaagcttcga ggcccagcga cctcggtggg cccagtgggg aggagcagga gcctgagcct   2393
tgggaacatg cgtgtgacct ccacagctac ctcttctatg gactggttgt tgccaaacag   2453
ccacactgtg ggactcttct taacttaaat tttaatttat ttatactatt tagttttttgt   2513
aatttatttt cgatttcaca gtgtgtttgt gattgtttgc tctgagagtt cccctgtccc   2573
ctcccccttc cctcacaccg cgtctggtga caaccgagtg gctgtcatca gcctgtgtag   2633
gcagtcatgg caccaaagcc accagactga caaatgtgta tcggatgctt ttgttcaggg   2693
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<210> 81
<211> 1085
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (329)...(625)

<400> 81
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tcccgtgggg gtgtggctag gctaagcgtt ttgagctgca ttgctgcgtg cttgatgctt   180
gtccttttg atcgtggtga tttagagggt gaactcactg gaatggggat gcttgcatgt   240
gtaatcttac taagagctaa tagaaaggct aggaccaaac cagaaacctc caattctcat   300
gtggaagccc atgccctcac cctccaac atg aaa gcc tct gca gca ctt ctg   352
                                 Met Lys Ala Ser Ala Ala Leu Leu
                                  1               5

tgt ctg ctg ctc aca gca gct gct ttc agc ccc cag ggg ctt gct cag    400
Cys Leu Leu Leu Thr Ala Ala Ala Phe Ser Pro Gln Gly Leu Ala Gln
     10               15                  20

cca gtt ggg att aat act tca act acc tgc tgc tac aga ttt atc aat    448
Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe Ile Asn
 25               30                  35                      40

aag aaa atc cct aag cag agg ctg gag agc tac aga agg acc acc agt    496
Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr Ser
                 45                  50                  55
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34

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agc cac tgt ccc cgg gaa gct gta atc ttc aag acc aaa ctg gac aag      544
Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu Asp Lys
            60                  65                  70

gag atc tgt gct gac ccc aca cag aag tgg gtc cag gac ttt atg aag      592
Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe Met Lys
            75                  80                  85

cac ctg gac aag aaa acc caa act cca aag ctt tgaacattca tgactgaact     645
His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu
        90                  95

gaaacaagc catgacttga gaaacaaata atttgtatac cctgtccttt ctcagagtgg      705
ttctgagatt attttaatct aattctaagg aatatgagct ttatgtaata atgtgaatca     765
tggtttttct tagtagattt taaaagttat taatatttta atttaatctt ccatggattt     825
tggtgggttt tgaacataaa gccttggatg tatatgtcat ctcagtgctg taaaaactgt     885
gggatgctcc tcccttctct acctcatggg ggtattgtat aagtccttgc aagaatcagt     945
gcaaagattt gctttaattg ttaagatatg atgtccctat ggaagcatat tgttattata    1005
taattacata tttgcatatg tatgactccc aaattttcac ataaaataga tttttgtata    1065
acaaaaaaaa aaaaaaaaaa                                                 1085

<210> 82
<211> 775
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (84)...(359)

<400> 82
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cattccgtca cctgctcaga atc atg cag gtc tcc act gct gcc ctt gct gtc     113
                         Met Gln Val Ser Thr Ala Ala Leu Ala Val
                          1               5                   10

ctc ctc tgc acc atg gct ctc tgc aac cag ttc tct gca tca ctt gct      161
Leu Leu Cys Thr Met Ala Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala
                15                  20                  25

gct gac acg ccg acc gcc tgc tgc ttc agc tac acc tcc cgg cag att      209
Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile
            30                  35                  40

cca cag aat ttc ata gct gac tac ttt gag acg agc agc cag tgc tcc      257
Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser
            45                  50                  55

aag ccc ggt gtc atc ttc cta acc aag cga agc cgg cag gtc tgt gct      305
Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg Gln Val Cys Ala
        60                  65                  70

gac ccc agt gag gag tgg gtc cag aaa tat gtc agc gac ctg gag ctg      353
Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser Asp Leu Glu Leu
    75                  80                  85                  90

agt gcc tgaggggtcc agaagcttcg aggcccagcg acctcggtgg gcccagtggg        409
Ser Ala


gaggagcagg agcctgagcc ttgggaacat gcgtgtgacc tccacagcta cctcttctat      469
ggactggttg ttgccaaaca gccacactgt gggactcttc ttaacttaaa ttttaattta      529
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35

tttatactat ttagtttttg taatttattt tcgatttcac agtgtgtttg tgattgtttg   589
ctctgagagt tcccctgtcc cctccccctt ccctcacacc gcgtctggtg acaaccgagt   649
ggctgtcatc agcctgtgta ggcagtcatg gcaccaaagc caccagactg acaaatgtgt   709
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aaaggt   775

<210> 83
<211> 98
<212> PRT
<213> Homo sapiens

<400> 83
Met Lys Val Ser Ala Val Leu Leu Cys Leu Leu Leu Met Thr Ala Ala
1   5   10   15
Phe Asn Pro Gln Gly Leu Ala Gln Pro Asp Ala Leu Asn Val Pro Ser
                20   25   30
Thr Cys Cys Phe Thr Phe Ser Ser Lys Lys Ile Ser Leu Gln Arg Leu
            35   40   45
Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val Ile
    50   55   60
Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys
65   70   75   80
Trp Val Gln Asn Tyr Met Lys His Leu Gly Arg Lys Ala His Thr Leu
                85   90   95
Lys Thr

<210> 84
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A region within a peptide of a chemokine, a
      variant, or a derivative thereof.

<221> SITE
<222> 1
<223> Xaa is Ala or Leu

<221> SITE
<222> 4
<223> Xaa is Lys, Ser or Thr

<221> SITE
<222> 5
<223> Xaa is any amino acid

<221> SITE
<222> 6
<223> Xaa is Lys, Glu, Ser or Arg

<221> SITE
<222> 8
<223> Xaa is Val or Ile

<400> 84
Xaa Asp Pro Xaa Xaa Xaa Trp Xaa Gln
1   5

<210> 85
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> A chemokine variant

<400> 85
Cys Leu Asp Pro Lys Gln Lys Trp Ile Gln
 1   5   10